

SEQUENCE LISTING

<110> Guss, Bengt  
Nilsson, Martin  
Frykberg, Lars  
Flock, Jan-Ingmar  
Lindberg, Martin

<120> Fibrinogen Binding Protein Originating from  
Coagulase-Negative Staphylococcus

<130> guss 09/147405

<140> 09/147405

<141> 1999-04-01

<150> PCT/SE97/10191

<151> 1997-06-18

<150> SE 9602496-3

<151> 1996-06-20

<160> 15

I <170> PatentIn Ver. 2.0

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 1

caacaaccat ctcacacaac

20

<210> 2

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2

catcaaattg atatttccca tc

22

<210> 3  
<211> 18  
<212> DNA  
<213> Staphylococcus epidermidis

<220>  
<221> variation  
<222> (3)  
<223> n i s c o r t

<220>  
<221> variation  
<222> (6)  
<223> n i s c, t, a, o r g

<220>  
<221> variation  
<222> (9)  
<223> n i s c o r t

<220>  
<221> variation  
<222> (12)  
<223> n i s c, t, a, o r g

<220>  
<221> variation  
<222> (15)  
<223> n i s c o r t

<220>  
<221> variation  
<222> (18)  
<223> n i s c o r t

<400> 3  
gantcngant cnganagn

18

<210> 4  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 4  
aggtcaagga caaggtgac

19

<210> 5  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 5  
ccgatgaaaa tggaaagtat c

21

<210> 6  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

I  
<400> 6  
tccgttatct atactaaagt c

21

<210> 7  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 7  
actgatcatg atgactttag t

21

<210> 8  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 8  
gcggatccaa tcagtcaata aacaccgacg at 32

<210> 9  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 9  
cggaattctg ttcggactga tttggaagtt cc 32

<210> 10  
<211> 1781  
<212> DNA  
<213> Staphylococcus epidermidis

<220>  
<221> CDS  
<222> (3)..(1781)

Ii

<400> 10  
ac cac cac cac cac cac cac ccc tct agt gat gaa gaa aag aat gat 47  
His His His His His His Pro Ser Ser Asp Glu Glu Lys Asn Asp  
1 5 10 15  
gtg atc aat aat aat cag tca ata aac acc gac gat aat aac caa ata 95  
Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile  
20 25 30  
att aaa aaa gaa gaa acg aat aac tac gat ggc ata gaa aaa cgc tca 143  
Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser  
35 40 45  
gaa gat aga aca gag tca aca aca aat gta gat gaa aac gaa gca aca 191  
Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr  
50 55 60  
ttt tta caa aag acc cct caa gat aat act cat ctt aca gaa gaa gag 239  
Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu  
65 70 75  
gta aaa gaa tcc tca tca gtc gaa tcc tca aat tca tca att gat act 287

Val	Lys	Glu	Ser	Ser	Ser	Val	Glu	Ser	Ser	Asn	Ser	Ser	Ile	Asp	Thr		
80						85				90					95		
gcc	caa	caa	cca	tct	cac	aca	aca	ata	aat	aga	gaa	gaa	tct	gtt	caa	335	
Ala	Gln	Gln	Pro	Ser	His	Thr	Thr	Ile	Asn	Arg	Glu	Glu	Ser	Val	Gln		
				100					105					110			
aca	agt	gat	aat	gta	gaa	gat	tca	cac	gta	tca	gat	ttt	gct	aac	tct	383	
Thr	Ser	Asp	Asn	Val	Glu	Asp	Ser	His	Val	Ser	Asp	Phe	Ala	Asn	Ser		
			115					120					125				
aaa	ata	aaa	gag	agt	aac	act	gaa	tct	ggg	aaa	gaa	gag	aat	act	ata	431	
Lys	Ile	Lys	Glu	Ser	Asn	Thr	Glu	Ser	Gly	Lys	Glu	Glu	Asn	Thr	Ile		
		130					135					140					
gag	caa	cct	aat	aaa	gta	aaa	gaa	gat	tca	aca	aca	agt	cag	ccg	tct	479	
Glu	Gln	Pro	Asn	Lys	Val	Lys	Glu	Asp	Ser	Thr	Thr	Ser	Gln	Pro	Ser		
		145				150					155						
ggc	tat	aca	aat	ata	gat	gaa	aaa	att	tca	aat	caa	gat	gag	tta	tta	527	
Gly	Tyr	Thr	Asn	Ile	Asp	Glu	Lys	Ile	Ser	Asn	Gln	Asp	Glu	Leu	Leu		
160				165					170					175			
aat	tta	cca	ata	aat	gaa	tat	gaa	aat	aag	gct	aga	cca	tta	tct	aca	575	
Asn	Leu	Pro	Ile	Asn	Glu	Tyr	Glu	Asn	Lys	Ala	Arg	Pro	Leu	Ser	Thr		
				180					185				190				
aca	tct	gcc	caa	cca	tcg	att	aaa	cgt	gta	acc	gta	aat	caa	tta	gcg	623	
Thr	Ser	Ala	Gln	Pro	Ser	Ile	Lys	Arg	Val	Thr	Val	Asn	Gln	Leu	Ala		
			195				200						205				
gcg	gaa	caa	ggg	tcg	aat	gtt	aac	cat	tta	att	aaa	gtt	act	gat	caa	671	
Ala	Glu	Gln	Gly	Ser	Asn	Val	Asn	His	Leu	Ile	Lys	Val	Thr	Asp	Gln		
		210				215					220						
agt	att	act	gaa	gga	tat	gat	gat	agt	gaa	ggg	gtt	att	aaa	gca	cat	719	
Ser	Ile	Thr	Glu	Gly	Tyr	Asp	Asp	Ser	Glu	Gly	Val	Ile	Lys	Ala	His		
	225					230				235							
gat	gct	gaa	aac	tta	atc	tat	gat	gta	act	ttt	gaa	gta	gat	gat	aag	767	
Asp	Ala	Glu	Asn	Leu	Ile	Tyr	Asp	Val	Thr	Phe	Glu	Val	Asp	Asp	Lys		
240				245					250					255			
gtg	aaa	tct	ggg	gat	acg	atg	aca	gtg	gat	ata	gat	aag	aat	aca	gtt	815	
Val	Lys	Ser	Gly	Asp	Thr	Met	Thr	Val	Asp	Ile	Asp	Lys	Asn	Thr	Val		
			260					265					270				
cca	tca	gat	tta	acc	gat	agc	ttt	aca	ata	cca	aaa	ata	aaa	gat	aat	863	

II

Pro	Ser	Asp	Leu	Thr	Asp	Ser	Phe	Thr	Ile	Pro	Lys	Ile	Lys	Asp	Asn		
			275					280					285				
tct	gga	gaa	atc	atc	gct	aca	ggt	act	tat	gat	aac	aaa	aat	aaa	caa	911	
Ser	Gly	Glu	Ile	Ile	Ala	Thr	Gly	Thr	Tyr	Asp	Asn	Lys	Asn	Lys	Gln		
		290					295				300						
atc	acc	tat	act	ttt	aca	gat	tat	gta	gat	aag	tat	gaa	aat	att	aaa	959	
Ile	Thr	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asp	Lys	Tyr	Glu	Asn	Ile	Lys		
	305					310				315							
gca	cac	ctt	aaa	tta	acg	tca	tac	att	gat	aaa	tca	aag	gtt	cca	aat	1007	
Ala	His	Leu	Lys	Leu	Thr	Ser	Tyr	Ile	Asp	Lys	Ser	Lys	Val	Pro	Asn		
320					325				330					335			
aat	aat	acc	aag	tta	gat	gta	gaa	tat	aaa	acg	gcc	ctt	tca	tca	gta	1055	
Asn	Asn	Thr	Lys	Leu	Asp	Val	Glu	Tyr	Lys	Thr	Ala	Leu	Ser	Ser	Val		
			340				345				350						
aat	aaa	aca	att	acg	gtt	gaa	tat	caa	aga	cct	aac	gaa	aat	cgg	act	1103	
Asn	Lys	Thr	Ile	Thr	Val	Glu	Tyr	Gln	Arg	Pro	Asn	Glu	Asn	Arg	Thr		
		355					360				365						
gct	aac	ctt	caa	agt	atg	ttt	aca	aat	ata	gat	acg	aaa	aat	cat	aca	1151	
Ala	Asn	Leu	Gln	Ser	Met	Phe	Thr	Asn	Ile	Asp	Thr	Lys	Asn	His	Thr		
		370				375				380							
gtt	gag	caa	acg	att	tat	att	aac	cct	ctt	cgt	tat	tca	gcc	aag	gaa	1199	
Val	Glu	Gln	Thr	Ile	Tyr	Ile	Asn	Pro	Leu	Arg	Tyr	Ser	Ala	Lys	Glu		
	385					390				395							
aca	aat	gta	aat	att	tca	ggg	aat	ggt	gat	gaa	ggt	tca	aca	att	ata	1247	
Thr	Asn	Val	Asn	Ile	Ser	Gly	Asn	Gly	Asp	Glu	Gly	Ser	Thr	Ile	Ile		
400					405				410					415			
gac	gat	agc	aca	ata	att	aaa	gtt	tat	aag	gtt	gga	gat	aat	caa	aat	1295	
Asp	Asp	Ser	Thr	Ile	Ile	Lys	Val	Tyr	Lys	Val	Gly	Asp	Asn	Gln	Asn		
			420					425			430						
tta	cca	gat	agt	aac	aga	att	tat	gat	tac	agt	gaa	tat	gaa	gat	gtc	1343	
Leu	Pro	Asp	Ser	Asn	Arg	Ile	Tyr	Asp	Tyr	Ser	Glu	Tyr	Glu	Asp	Val		
		435					440				445						
aca	aat	gat	gat	tat	gcc	caa	tta	gga	aat	aat	aat	gat	gtg	aat	att	1391	
Thr	Asn	Asp	Asp	Tyr	Ala	Gln	Leu	Gly	Asn	Asn	Asn	Asp	Val	Asn	Ile		
		450					455				460						
aat	ttt	ggt	aat	ata	gat	tca	cca	tat	att	att	aaa	gtt	att	agt	aaa	1439	

Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys	
465 470 475	
tat gac cct aat aag gat gat tac acg act ata cag caa act gtg aca	1487
Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr	
480 485 490 495	
atg cag acg act ata aat gag tat act ggt gag ttt aga aca gca tcc	1535
Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser	
500 505 510	
tat gat aat aca att gct ttc tct aca agt tca ggt caa gga caa ggt	1583
Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly	
515 520 525	
gac ttg cct cct gaa aaa act tat aaa atc gga gat tac gta tgg gaa	1631
Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu	
530 535 540	
gat gta gat aaa gat ggt att caa aat aca aat gat aat gaa aaa ccg	1679
Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro	
545 550 555	
ctt agt aat gta ttg gta act ttg acg tat cct gat gga act tca aaa	1727
Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys	
560 565 570 575	
tca gtc aga aca gat gaa gat ggg aaa tat caa ttt gat ggg gtg cag	1775
Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly Val Gln	
580 585 590	
gtc gac	1781
Val Asp	

<210> 11  
 <211> 593  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 11  
 His His His His His His Pro Ser Ser Asp Glu Glu Lys Asn Asp Val  
 1 5 10 15  
 Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile  
 20 25 30  
 Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu

35                      40                      45  
 Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe  
     50                      55                      60  
 Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val  
     65                      70                      75                      80  
 Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala  
                             85                      90                      95  
 Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr  
                             100                      105                      110  
 Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys  
                             115                      120                      125  
 Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu  
     130                      135                      140  
 Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly  
     145                      150                      155                      160  
 Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn  
                             165                      170                      175  
 Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr  
                             180                      185                      190  
 Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala  
                             195                      200                      205  
 Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser  
     210                      215                      220  
 Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp  
     225                      230                      235                      240  
 Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val  
                             245                      250                      255  
 Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val Pro  
                             260                      265                      270  
 Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn Ser  
                             275                      280                      285  
 Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile



290                      295                      300  
 Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala  
 305                      310                      315                      320  
 His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn  
                          325                      330                      335  
 Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn  
                          340                      345                      350  
 Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr Ala  
                          355                      360                      365  
 Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr Val  
                          370                      375                      380  
 Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr  
 385                      390                      395                      400  
 Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp  
                          405                      410                      415  
 Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn Leu  
                          420                      425                      430  
 Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr  
                          435                      440                      445  
 Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile Asn  
                          450                      455                      460  
 Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr  
 465                      470                      475                      480  
 Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr Met  
                          485                      490                      495  
 Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr  
                          500                      505                      510  
 Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp  
                          515                      520                      525  
 Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp  
                          530                      535                      540  
 Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu

545		550		555		560
Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser						
	565		570		575	
Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly Val Gln Val						
	580		585		590	

Asp

<210> 12  
 <211> 1746  
 <212> DNA  
 <213> Staphylococcus epidermidis

<400> 12  
 tctagtgatg aagaaaagaa tgatgtgatc aataataatc agtcaataaa caccgacgat 60  
 aataaccaa taattaaaaa agaagaaacg aataactacg atggcataga aaaacgctca 120  
 gaagatagaa cagagtcaac aacaaatgta gatgaaaacg aagcaacatt ttacaaaaag 180  
 acccctcaag ataataactca tcttacagaa gaagaggtaa aagaatctc atcagtcgaa 240  
 tcctcaaatt catcaattga tactgcccaa caaccatctc acacaacaat aaatagagaa 300  
 gaatctgttc aaacaagtga taatgtagaa gattcacacg tatcagattt tgctaactct 360  
 aaaataaaa agagtaacac tgaatctggt aaagaagaga atactataga gcaacctaat 420  
 aaagtaaaag aagattcaac aacaagtcag ccgtctggct atacaaatat agatgaaaaa 480  
 atttcaaadc aagatgagtt attaaattta ccaataaatg aatatgaaaa taaggctaga 540  
 ccattatcta caacatctgc ccaaccatcg attaaacgtg taaccgtaaa tcaattagcg 600  
 gcggaacaag gttcgaatgt taaccattta attaaagtta ctgatcaaag tattactgaa 660  
 ggatatgatg atagtgaagg tgttattaaa gcacatgatg ctgaaaactt aatctatgat 720  
 gtaacttttg aagtagatga taagggtgaaa tctgggtgata cgatgacagt ggatatagat 780  
 aagaatacag ttccatcaga tttaaccgat agctttacaa taccaaaaat aaaagataat 840  
 tctggagaaa tcatcgctac aggtacttat gataacaaaa ataaacaaat cacctatact 900

tttacagatt atgtagataa gtatgaaaat attaaagcac accttaaatt aacgtcatac 960  
 attgataaat caaagggttcc aaataataat accaagttag atgtagaata taaaacggcc 1020  
 ctttcatcag taaataaaac aattacggtt gaatatcaaa gacctaacga aaatcggact 1080  
 gctaaccttc aaagtatggt tacaatatata gatacgaaaa atcatacagt tgagcaaacg 1140  
 atttatatta accctcttcg ttattcagcc aaggaaacaa atgtaaatat ttcagggaat 1200  
 ggtgatgaag gttcaacaat tatagacgat agcacaataa ttaaagttta taagggttga 1260  
 gataatcaaa atttaccaga tagtaacaga atttatgatt acagtgaata tgaagatgtc 1320  
 acaaagatg attatgccca attaggaaat aataatgatg tgaatattaa ttttggtaat 1380  
 atagattcac catatattat taaagttatt agtaaatatg accctaataa ggatgattac 1440  
 acgactatac agcaaactgt gacaatgcag acgactataa atgagtatac tgggtgagttt 1500  
 agaacagcat cctatgataa tacaattgct ttctctacaa gttcaggtca aggacaaggt 1560  
 gacttgctc ctgaaaaaac ttataaaatc ggagattacg tatgggaaga tntagataaa 1620  
 gatggtattc aaaatacaaa tgataatgaa aaaccgctta gtaatgtatt ggtaactttg 1680  
 acgtatcctg atggaacttc aaaatcagtc agaacagatg aagatgggaa atatcaattt 1740  
 gatgga 1746

<210> 13  
 <211> 582  
 <212> PRT  
 <213> Staphylococcus epidermidis

<400> 13  
 Ser Ser Asp Glu Glu Lys Asn Asp Val Ile Asn Asn Asn Gln Ser Ile  
 1 5 10 15  
 Asn Thr Asp Asp Asn Asn Gln Ile Ile Lys Lys Glu Glu Thr Asn Asn  
 20 25 30  
 Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr  
 35 40 45  
 Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp  
 50 55 60

Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser Ser Val Glu  
 65 70 75 80  
 Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser His Thr Thr  
 85 90 95  
 Ile Asn Arg Glu Glu Ser Val Gln Thr Ser Asp Asn Val Glu Asp Ser  
 100 105 110  
 His Val Ser Asp Phe Ala Asn Ser Lys Ile Lys Glu Ser Asn Thr Glu  
 115 120 125  
 Ser Gly Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Lys Glu  
 130 135 140  
 Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile Asp Glu Lys  
 145 150 155 160  
 Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr Glu  
 165 170 175  
 Asn Lys Ala Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ile Lys  
 180 185 190  
 Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val Asn  
 195 200 205  
 His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp Asp  
 210 215 220  
 Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr Asp  
 225 230 235 240  
 Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met Thr  
 245 250 255  
 Val Asp Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr Asp Ser Phe  
 260 265 270  
 Thr Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr Gly  
 275 280 285  
 Thr Tyr Asp Asn Lys Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp Tyr  
 290 295 300  
 Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu Thr Ser Tyr  
 305 310 315 320

Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val Glu  
325 330 335

Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu Tyr  
340 345 350

Gln Arg Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe Thr  
355 360 365

Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile Asn  
370 375 380

Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly Asn  
385 390 395 400

Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys Val  
405 410 415

Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr  
420 425 430

Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu  
435 440 445

Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro  
450 455 460

Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr  
465 470 475 480

Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu Tyr  
485 490 495

Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser  
500 505 510

Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr Tyr  
515 520 525

Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile Gln  
530 535 540

Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr Leu  
545 550 555 560

Thr Tyr Pro Asp Gly Thr Ser Lys Ser Val Arg Thr Asp Glu Asp Gly  
565 570 575

Lys Tyr Gln Phe Asp Gly  
580

new

<210> 14  
<211> 3600  
<212> DNA  
<213> Staphylococcus epidermidis

<220>  
<221> CDS  
<222> (33)..(3308)

<400> 14  
tacattgaaa tagtcaaaga aaaggagttt tt atg att aat aaa aaa aat aat 53  
Met Ile Asn Lys Lys Asn Asn  
1 5  
  
tta cta act aaa aag aaa cct ata gca aat aaa tcc aat aaa tat gca 101  
Leu Leu Thr Lys Lys Lys Pro Ile Ala Asn Lys Ser Asn Lys Tyr Ala  
10 15 20  
  
att aga aaa ttc aca gta ggt aca gcg tct att gta ata ggt gca aca 149  
Ile Arg Lys Phe Thr Val Gly Thr Ala Ser Ile Val Ile Gly Ala Thr  
25 30 35  
  
tta ttg ttt ggt tta ggt cat aat gag gcc aaa gcc gag gag aat tca 197  
Leu Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Ser  
40 45 50 55  
  
gta caa gac gtt aaa gat tcg aat acg gat gat gaa tta tca gac agc 245  
Val Gln Asp Val Lys Asp Ser Asn Thr Asp Asp Glu Leu Ser Asp Ser  
60 65 70  
  
aat gat cag tct agt gat gaa gaa aag aat gat gtg atc aat aat aat 293  
Asn Asp Gln Ser Ser Asp Glu Glu Lys Asn Asp Val Ile Asn Asn Asn  
75 80 85  
  
cag tca ata aac acc gac gat aat aac caa ata att aaa aaa gaa gaa 341  
Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile Lys Lys Glu Glu  
90 95 100  
  
acg aat aac tac gat ggc ata gaa aaa cgc tca gaa gat aga aca gag 389  
Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu  
105 110 115  
  
tca aca aca aat gta gat gaa aac gaa gca aca ttt tta caa aag acc 437

Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr	
120 125 130 135	
cct caa gat aat act cat ctt aca gaa gaa gag gta aaa gaa tcc tca	485
Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser	
140 145 150	
tca gtc gaa tcc tca aat tca tca att gat act gcc caa caa cca tct	533
Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser	
155 160 165	
cac aca aca ata aat aga gaa gaa tct gtt caa aca agt gat aat gta	581
His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr Ser Asp Asn Val	
170 175 180	
gaa gat tca cac gta tca gat ttt gct aac tct aaa ata aaa gag agt	629
Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys Ile Lys Glu Ser	
185 190 195	
aac act gaa tct ggt aaa gaa gag aat act ata gag caa cct aat aaa	677
Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys	
200 205 210 215	
gta aaa gaa gat tca aca aca agt cag ccg tct ggc tat aca aat ata	725
Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile	
220 225 230	
gat gaa aaa att tca aat caa gat gag tta tta aat tta cca ata aat	773
Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn	
235 240 245	
gaa tat gaa aat aag gct aga cca tta tct aca aca tct gcc caa cca	821
Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro	
250 255 260	
tcg att aaa cgt gta acc gta aat caa tta gcg gcg gaa caa ggt tcg	869
Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser	
265 270 275	
aat gtt aac cat tta att aaa gtt act gat caa agt att act gaa gga	917
Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly	
280 285 290 295	
tat gat gat agt gaa ggt gtt att aaa gca cat gat gct gaa aac tta	965
Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu	
300 305 310	
atc tat gat gta act ttt gaa gta gat gat aag gtg aaa tct ggt gat	1013

Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp	
315 320 325	
acg atg aca gtg gat ata gat aag aat aca gtt cca tca gat tta acc	1061
Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr	
330 335 340	
gat agc ttt aca ata cca aaa ata aaa gat aat tct gga gaa atc atc	1109
Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile	
345 350 355	
gct aca ggt act tat gat aac aaa aat aaa caa atc acc tat act ttt	1157
Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile Thr Tyr Thr Phe	
360 365 370 375	
aca gat tat gta gat aag tat gaa aat att aaa gca cac ctt aaa tta	1205
Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu	
380 385 390	
acg tca tac att gat aaa tca aag gtt cca aat aat aat acc aag tta	1253
Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu	
395 400 405	
gat gta gaa tat aaa acg gcc ctt tca tca gta aat aaa aca att acg	1301
Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr	
410 415 420	
gtt gaa tat caa aga cct aac gaa aat cgg act gct aac ctt caa agt	1349
Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser	
425 430 435	
atg ttt aca aat ata gat acg aaa aat cat aca gtt gag caa acg att	1397
Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile	
440 445 450 455	
tat att aac cct ctt cgt tat tca gcc aag gaa aca aat gta aat att	1445
Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile	
460 465 470	
tca ggg aat ggt gat gaa ggt tca aca att ata gac gat agc aca ata	1493
Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile	
475 480 485	
att aaa gtt tat aag gtt gga gat aat caa aat tta cca gat agt aac	1541
Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn	
490 495 500	
aga att tat gat tac agt gaa tat gaa gat gtc aca aat gat gat tat	1589



Arg	Ile	Tyr	Asp	Tyr	Ser	Glu	Tyr	Glu	Asp	Val	Thr	Asn	Asp	Asp	Tyr		
505						510					515						
gcc	caa	tta	gga	aat	aat	aat	gat	gtg	aat	att	aat	ttt	ggt	aat	ata	1637	
Ala	Gln	Leu	Gly	Asn	Asn	Asn	Asp	Val	Asn	Ile	Asn	Phe	Gly	Asn	Ile		
520					525				530					535			
gat	tca	cca	tat	att	att	aaa	gtt	att	agt	aaa	tat	gac	cct	aat	aag	1685	
Asp	Ser	Pro	Tyr	Ile	Ile	Lys	Val	Ile	Ser	Lys	Tyr	Asp	Pro	Asn	Lys		
				540					545					550			
gat	gat	tac	acg	act	ata	cag	caa	act	gtg	aca	atg	cag	acg	act	ata	1733	
Asp	Asp	Tyr	Thr	Thr	Ile	Gln	Gln	Thr	Val	Thr	Met	Gln	Thr	Thr	Ile		
			555					560					565				
aat	gag	tat	act	ggt	gag	ttt	aga	aca	gca	tcc	tat	gat	aat	aca	att	1781	
Asn	Glu	Tyr	Thr	Gly	Glu	Phe	Arg	Thr	Ala	Ser	Tyr	Asp	Asn	Thr	Ile		
		570					575					580					
gct	ttc	tct	aca	agt	tca	ggt	caa	gga	caa	ggt	gac	ttg	cct	cct	gaa	1829	
Ala	Phe	Ser	Thr	Ser	Ser	Gly	Gln	Gly	Gln	Gly	Asp	Leu	Pro	Pro	Glu		
	585					590					595						
aaa	act	tat	aaa	atc	gga	gat	tac	gta	tgg	gaa	gat	gta	gat	aaa	gat	1877	
Lys	Thr	Tyr	Lys	Ile	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Val	Asp	Lys	Asp		
600					605					610				615			
ggt	att	caa	aat	aca	aat	gat	aat	gaa	aaa	ccg	ctt	agt	aat	gta	ttg	1925	
Gly	Ile	Gln	Asn	Thr	Asn	Asp	Asn	Glu	Lys	Pro	Leu	Ser	Asn	Val	Leu		
				620					625					630			
gta	act	ttg	acg	tat	cct	gat	gga	act	tca	aaa	tca	gtc	aga	aca	gat	1973	
Val	Thr	Leu	Thr	Tyr	Pro	Asp	Gly	Thr	Ser	Lys	Ser	Val	Arg	Thr	Asp		
				635				640					645				
gaa	gat	ggg	aaa	tat	caa	ttt	gat	gga	ttg	aaa	aac	gga	ttg	act	tat	2021	
Glu	Asp	Gly	Lys	Tyr	Gln	Phe	Asp	Gly	Leu	Lys	Asn	Gly	Leu	Thr	Tyr		
		650					655					660					
aaa	att	aca	ttc	gaa	aca	cct	gaa	gga	tat	acg	ccg	acg	ctt	aaa	cat	2069	
Lys	Ile	Thr	Phe	Glu	Thr	Pro	Glu	Gly	Tyr	Thr	Pro	Thr	Leu	Lys	His		
		665				670						675					
tca	gga	aca	aat	cct	gca	cta	gac	tca	gaa	ggt	aat	tct	gta	tgg	gta	2117	
Ser	Gly	Thr	Asn	Pro	Ala	Leu	Asp	Ser	Glu	Gly	Asn	Ser	Val	Trp	Val		
					685					690					695		
act	att	aat	gga	caa	gac	gat	atg	acg	att	gat	agt	gga	ttt	tat	caa	2165	

I

Thr	Ile	Asn	Gly	Gln	Asp	Asp	Met	Thr	Ile	Asp	Ser	Gly	Phe	Tyr	Gln		
				700					705					710			
aca	cct	aaa	tac	agc	tta	ggg	aac	tat	gta	tgg	tat	gac	act	aat	aaa		2213
Thr	Pro	Lys	Tyr	Ser	Leu	Gly	Asn	Tyr	Val	Trp	Tyr	Asp	Thr	Asn	Lys		
			715					720					725				
gat	ggg	att	caa	ggg	gat	gat	gaa	aaa	gga	atc	tct	gga	gtt	aaa	gtg		2261
Asp	Gly	Ile	Gln	Gly	Asp	Asp	Glu	Lys	Gly	Ile	Ser	Gly	Val	Lys	Val		
			730				735					740					
acg	tta	aaa	gat	gaa	aac	gga	aat	atc	att	agt	aca	act	aca	acc	gat		2309
Thr	Leu	Lys	Asp	Glu	Asn	Gly	Asn	Ile	Ile	Ser	Thr	Thr	Thr	Thr	Asp		
			745			750					755						
gaa	aat	gga	aag	tat	caa	ttt	gat	aat	tta	aat	agt	ggg	aat	tat	att		2357
Glu	Asn	Gly	Lys	Tyr	Gln	Phe	Asp	Asn	Leu	Asn	Ser	Gly	Asn	Tyr	Ile		
760					765				770					775			
gtt	cat	ttt	gat	aaa	cct	tca	ggg	atg	act	caa	aca	aca	aca	gat	tct		2405
Val	His	Phe	Asp	Lys	Pro	Ser	Gly	Met	Thr	Gln	Thr	Thr	Thr	Asp	Ser		
				780				785						790			
ggg	gat	gat	gac	gaa	cag	gat	gct	gat	ggg	gaa	gaa	gtt	cat	gta	aca		2453
Gly	Asp	Asp	Asp	Glu	Gln	Asp	Ala	Asp	Gly	Glu	Glu	Val	His	Val	Thr		
				795			800						805				
att	act	gat	cat	gat	gac	ttt	agt	ata	gat	aac	gga	tac	tat	gat	gac		2501
Ile	Thr	Asp	His	Asp	Asp	Phe	Ser	Ile	Asp	Asn	Gly	Tyr	Tyr	Asp	Asp		
			810				815					820					
gaa	tcg	gat	tcc	gat	agt	gac	tca	gac	agc	gac	tca	gat	tcc	gat	agt		2549
Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser		
			825			830					835						
gat	tca	gac	tcc	gat	agc	gac	tcg	gat	tca	gac	agc	gac	tca	gat	tca		2597
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser		
840					845				850					855			
gac	agc	gac	tcg	gat	tct	gat	agc	gac	tcg	gat	tca	gac	agc	gac	tca		2645
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser		
				860				865					870				
gac	tca	gac	agt	gat	tca	gat	tca	gac	agc	gac	tca	gat	tcc	gat	agt		2693
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser		
			875				880						885				
gat	tca	gac	tca	gac	agc	gac	tca	gat	tct	gat	agt	gat	tca	gac	tca		2741

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser	
890 895 900	
gac agt gat tca gat tca gac agc gac tca gat tcc gat agt gat tca	2789
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser	
905 910 915	
gac tca gac agc gac tca gat tcc gat agt gat tca gac tca gac agc	2837
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser	
920 925 930 935	
gac tca gat tct gat agt gat tca gac tca gac agt gat tca gac tca	2885
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser	
940 945 950	
gac agt gat tca gat tcc gat agt gat tca gac tcc gat agc gac tca	2933
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser	
955 960 965	
gac tcg gat agt gac tca gat tct gat agt gat tca gac tcc gat agc	2981
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser	
970 975 980	
gac tca gac tcg gat agt gac tca gat tct gat agt gat tca gac tca	3029
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser	
985 990 995	
gac agc gac tca gat tct gat agt gat tca gac tca gtc agt gat tca	3077
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Val Ser	
1000 1005 1010 1015	
gat tcc gat agt gat tca gac tca ggc agt gat tcg gat tcc gat agt	3125
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp Ser	
1020 1025 1030	
gat tca gac tca gac aac gac tca gat tta ggc aat agc tca gat aag	3173
Asp Ser Asp Ser Asp Asn Asp Ser Asp Leu Gly Asn Ser Ser Asp Lys	
1035 1040 1045	
agt aca aaa gat aaa tta cct gat aca gga gct aat gaa gat tat ggc	3221
Ser Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp Tyr Gly	
1050 1055 1060	
tct aaa ggc acg tta ctt gga act ctg ttt gca ggt tta gga gcg tta	3269
Ser Lys Gly Thr Leu Leu Gly Thr Leu Phe Ala Gly Leu Gly Ala Leu	
1065 1070 1075	
tta tta ggg aaa cgt cgc aaa aat aga aaa aat aaa aat taaaatgttc	3318

Leu Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn  
1080 1085 1090

aaatgaaatt tgtagaaaga agcagatatg agatttgaat agaaagtaga tttagtccaa 3378  
caaatgtaag atgttgatta aaactataat ataactttca cgtttatcat atcttgtaga 3438  
aaagatgatg caaacaaggt catttctatt aaaaatgact taaatgtatg atttttagag 3498  
aaacatatac aactcacaat ctgacaatga ttaatatagag gaaccgtgaa ttttaaataa 3558  
attcatgggt ccttttttatt gaattaataa aaattctttt at 3600

<210> 15

<211> 1092

<212> PRT

<213> Staphylococcus epidermidis

<400> 15

Met Ile Asn Lys Lys Asn Asn Leu Leu Thr Lys Lys Lys Pro Ile Ala  
1 5 10 15

Asn Lys Ser Asn Lys Tyr Ala Ile Arg Lys Phe Thr Val Gly Thr Ala  
20 25 30

Ser Ile Val Ile Gly Ala Thr Leu Leu Phe Gly Leu Gly His Asn Glu  
35 40 45

Ala Lys Ala Glu Glu Asn Ser Val Gln Asp Val Lys Asp Ser Asn Thr  
50 55 60

Asp Asp Glu Leu Ser Asp Ser Asn Asp Gln Ser Ser Asp Glu Glu Lys  
65 70 75 80

Asn Asp Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn  
85 90 95

Gln Ile Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys  
100 105 110

Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu  
115 120 125

Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu  
130 135 140

Glu Glu Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile



405 410 415  
 Ser Val Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn  
 420 425 430  
 Arg Thr Ala Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn  
 435 440 445  
 His Thr Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala  
 450 455 460  
 Lys Glu Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr  
 465 470 475 480  
 Ile Ile Asp Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn  
 485 490 495  
 Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu  
 500 505 510  
 Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val  
 515 520 525  
 Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile  
 530 535 540  
 Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr  
 545 550 555 560  
 Val Thr Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr  
 565 570 575  
 Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly  
 580 585 590  
 Gln Gly Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val  
 595 600 605  
 Trp Glu Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu  
 610 615 620  
 Lys Pro Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr  
 625 630 635 640  
 Ser Lys Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly  
 645 650 655  
 Leu Lys Asn Gly Leu Thr Tyr Lys Ile Thr Phe Glu Thr Pro Glu Gly



915

920

925

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
930 935 940

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
945 950 955 960

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
965 970 975

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
980 985 990

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
995 1000 1005

Ser Asp Ser Val Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Gly  
1010 1015 1020

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Asn Asp Ser Asp  
1025 1030 1035 1040

Leu Gly Asn Ser Ser Asp Lys Ser Thr Lys Asp Lys Leu Pro Asp Thr  
1045 1050 1055

Gly Ala Asn Glu Asp Tyr Gly Ser Lys Gly Thr Leu Leu Gly Thr Leu  
1060 1065 1070

Phe Ala Gly Leu Gly Ala Leu Leu Leu Gly Lys Arg Arg Lys Asn Arg  
1075 1080 1085

Lys Asn Lys Asn  
1090